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Prediction of heart disease using random forest algorithm, support vector machine, and neural network

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ABSTRACT

The heart is a vital organ responsible for pumping blood throughout the human body. Machine learning has become an increasingly important tool in medical forecasting, improving diagnostic accuracy and reducing human errors. This study focuses on detecting heart disease using machine learning algorithms. It aims to compare the performance of three key algorithms random forest (RF), support vector machine (SVM), and neural networks (NN), in predicting heart disease. Using a patient dataset with both nominal and numeric attributes, record mining techniques were applied through Orange software. The target classes indicated the absence (0) or presence (1) of heart disorders. The evaluation was based on the prediction accuracy of each algorithm. Results show that SVM achieved the highest accuracy, with a rate of 85%, outperforming RF and NN. The findings suggest that the SVM algorithm is a reliable tool for heart disease prediction, helping reduce diagnostic errors and improve medical decision-making.

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1. INTRODUCTION

Smart health system as "the result of a natural synergy between m-health and smart cities, from an information and communication technology (ICT) perspective as well as individuals and communities", m-Health stands for healthcare services via mobile devices [1]. Several implementations of e-Healt and m-Health are being developed continuously to implement a prediction system and find the best algorithm for several diseases, especially heart disease. The coronary heart is a essential organ that is owned by humans, and it pumps blood throughout the body. If the heart is problematic then humans will get many diseases that attack the body, therefore humans must have a healthy heart.

Under relaxed conditions, the normal heart rate of humans over the age of 18 is generally between 60 beats per minute (BPM) to 100 BPM, pumping about 2,000 gallons of blood every day and it is the most

important organ in the human body. Chronic heart disease and disease progression occurs when the heart cannot supply sufficient blood to tissues and organs at physiological filling pressures to meet metabolic needs. Despite advances in medicine and the healthcare industry, the five-year survival rate for people affected by heart disease is around 50% [2], [3]. The development of heart disease is one causes disability disruption of balance between blood supply and demand that occurs due to blockage of blood vessels [4], [5]. This category of heart disease is called circulatory disease. Various types of heart disease including congenital heart disease, dilated cardiomyopathy, heart failure, coronary artery disease, myocardial infarction, mitral regurgitation, hypertrophic cardiomyopathy, arrhythmia [6]. The death rate from heart disease is among the highest in the world.

Lack of skilled doctors and ignoring the patient's symptoms causes great challenges that can lead to death, not good for patients [7], [8]. Therefore, an information system is needed analysis tool to find hidden patterns in heart disorder data. Data minning is a cognitive process to find hidden proximal patterns in large amounts of data [9], [10]. Here, various techniques are listed and tested to determine the accuracy level of each. In previous studies, researchers have expressed efforts to find the best predictive model. The use of machine learning is rapidly increasing in the medical diagnostics industry as computer analysis reduces manual errors and improves accuracy [11]. Using machine learning techniques, disease diagnosis becomes highly reliable [12].

Medical data mining is a very important research area, it has contributed to the development of various applications in the growing healthcare field [13], [14]. Data mining is the search for useful information from very large sets of data. Some of the most important and common techniques for data mining include association rules, classification, clustering, prediction, and sequential models [15]. Data mining techniques are used for various applications. Data mining plays an important role in disease detection in healthcare. Patients should be asked to undergo a series of tests for the disease, although data mining techniques may be used to reduce the number of tests.

It has been stated in the literature that applying technical features and feature selection improves both classification and prediction results. Various machine learning and deep learning techniques are used to detect cardiac disease and hyperparameter optimization is performed to increase the accuracy of the results. Neural networks (NN) achieve a high accuracy of 78.3 percent and other models include ensemble techniques such as logistic regression, support vector machine (SVM), and random forest (RF) to mitigate cardiovascular features [16]. Various data mining techniques can be used to analyze cardiac related problems. There are various types of data mining techniques such as decision trees (DT), Naïve Bayes (NB), SVM, K-nearest neighbor (K-NN) classifiers, hybrid approaches, and artificial neural networks (ANN). Classification algorithms such as NB, DT, and ANN have been widely used in predicting heart diseases and have achieved different levels of accuracy [17], [18].

This study compares the results of the best algorithms from several previous studies, RF algorithm, SVM, and ANN, to get the best algorithm for predicting heart disease. The main objective of this study was to identify the best classification algorithm from previous studies conducted by [12]. For this reason, data mining techniques are carried out by comparing three data mining classification algorithms, namely the RF algorithm, SVM, and NN.

2. METHOD

This research involves an investigation of the treatment of parameters and variables which all depend on the researcher himself. Heart disease dataset from the latest University of California, Invene (UCI) repository on September 11, 2021. UCI machine learning consists of four databases extracting information from Hungary, Cleveland, Long Beach, Virginia, and Switzerland. A total of 918 datasets with a total of 76 attributes are included, but a subset of 12 attributes was used in the experiments. These attributes are categorical, real-valued, and integer-valued. The dataset attributes can be seen as in Table 1.

The collection of research literature from articles or journals adapted to this research is the prediction of heart disease. For the next step is choosing models or algorithms from previous studies, namely the RF algorithm, SVM and NN. Furthermore, training for the dataset is given, then prediction evaluation with area under the curve (AUC), component analysis (CA), F1, precision, recall, confusion matrix and receiver operating characteristic (ROC) analysis. The process can be seen in Figure 1. The data mining process written in Figure 1 is implemented using the Orange application as shown in Figure 2.

Table 1. Attributes of the heart disease dataset [11]

Attribute	Information attribute	Description
Age	Integer	Age in years (29 to 77)
Sex	Integer	Gender instance (0=Female, 1=Male)
ChestPainType	Integer	Chest pain type (1: typical angina, 2: atypical angina, 3: non-anginal pain, and 4:asymptomatic)
RestingBP	Integer	Resting blood pressure in mm Hg
Cholesterol	Integer	Serum cholesterol in mg/dl
FastingBS	Integer	Fasting blood sugar >120 mg/dl (0=False, 1=True)
RestingECG	Integer	Resting ECG results (0: normal, 1: ST-Twave abnormality, 2: LV hypertrophy)
MaxHR	Integer	Maximum heart rate achieved
ExerciseAngina	Integer	Exercise induced angina (0: No, 1: Yes)
Oldpeak	Integer	ST depression induced by exercise relativeto rest [0.0, 62.0]
ST_Slope	Integer	Slope of the peak exe+A1:D13rcise ST segment (1: up-sloping, 2: flat, 3: down-sloping)
HeartDisease	Integer	Target

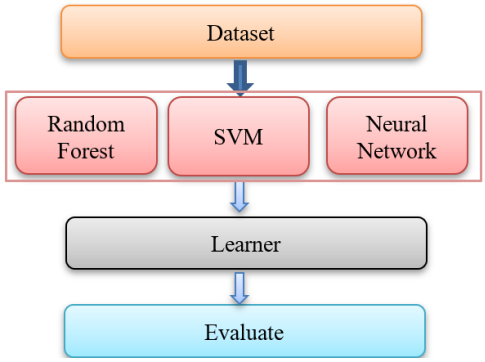


Figure 1. Data mining process

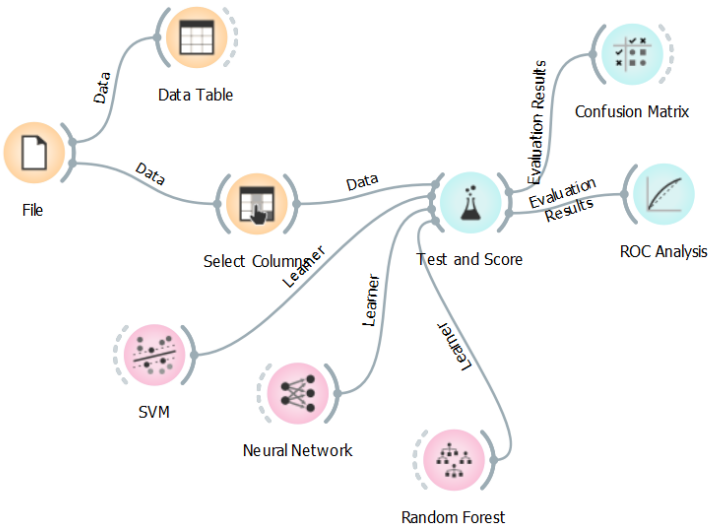


Figure 2. Workflow of heart disease prediction process

2.1. Random forest

The RF algorithm is a collection of classifiers for various tree types. Leo Breiman pioneered the use of randomized forests in formal studies. He explains how to generating a forest of unrelated trees in his work by combining the classification and regression treelike (CART-like) procedure with random node optimization and bagging. The Breiman algorithm aims to combine decisions from several rather than generating a single DT, multivariate trees, each trained on a different training cluster [19].

The RF algorithm uses several DT to determine the classification value during the classification process. Instead of dividing each node into branches based on the best branch among all variables, the RF algorithm divides each node into variables based on the best variable among the variables chosen at random in each node [20]. Each dataset is generated using data that has been moved from the original. Then, using the random selection feature, the tree is developed without pruning [21], [22].

2.2. Neural network

NNs are an attempt to mimic the functioning of the human brain. The human brain is thought to be made up of millions of small processing units called neurons that operate in parallel. The neurons are connected to each other by neuronal connections. Each neuron receives input from groups of these neurons, processes the input, and passes an output back to the group of neurons [23]. The output is collected by other neurons for further processing [24]. The quantity of enter neurons withinside the enter layer is 25 neurons, one hidden layer has 50 hidden neurons, and the output layer contains one neuron to determine the hypertension class (1) or not hypertension (0) with 1,000 epochs or iterations [25]. The hidden layer used in this research is 100.

2.3. Support vector machine

SVM is a guided learning method in classifying. SVM can be used in linear or non-linear classification [26]. The best hyperplane can be found by measuring the hyperplane margins and finding the maximum point [27]-[29]. Basically non-linear SVM is a solution to the linear SVM problem by performing kernel functions in a high-dimensional feature space [30].

Some of the performance metrics that are common and often used are as follows.

a. Accuracy

Accuracy can indicate how well a model classifies correctly. Therefore, prediction accuracy is the ratio of the number of true positives and true negatives to the whole data. In other words, accuracy is how close the predicted value is to the actual value. The value of accuracy can be seen in (1).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

b. Precision

Accuracy can be explained as the degree of accuracy of the requested data with the prediction results provided by the model. Therefore, accuracy can be interpreted as the ratio of correct positive predictions divided by the total positive prediction results. In other words, out of all the correctly predicted positive class data, how many data are actually positive? The value of accuracy can be seen in (2).

$$Presisi = \frac{TP}{TP+FP} \quad (2)$$

c. Recall

Recall or sensitivity can be described as the success of a model in retrieving information. Therefore, we can say that recall is the proportion of true positive predictions divided by the total number of true positives. The value of recall can be found in (3).

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

d. Specificity

Specificity refers to the accuracy of predicting negative data, divided by the total number of negative cases. It indicates how well a model correctly identifies negative instances. A higher specificity means the model is effective at minimizing false positives. Specificity is typically calculated in medical diagnostics to ensure that healthy individuals are not mistakenly classified as having a disease. The value of specificity can be found in (4).

$$Specificity = \frac{TN}{TN+F} \quad (4)$$

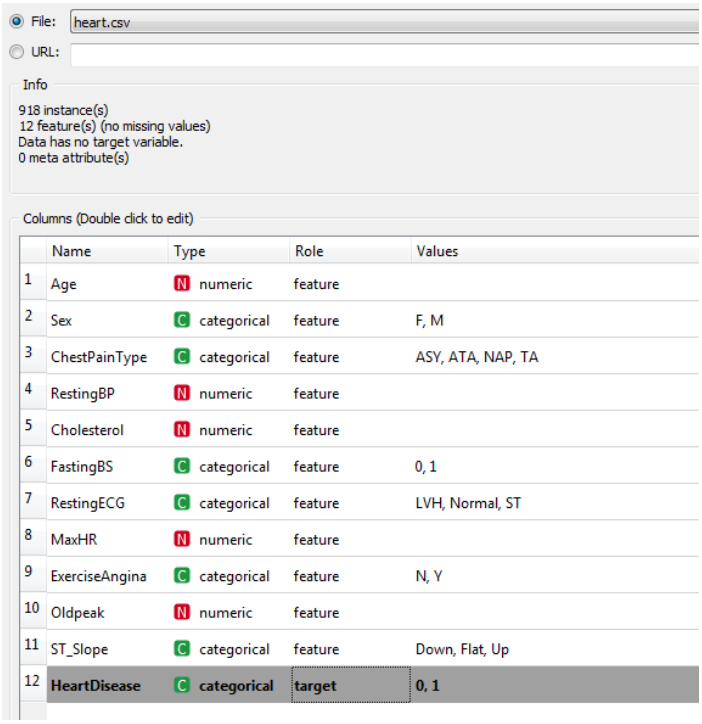
e. F1 score

F1 score is a weighted comparison of average precision and recall. F1 score is best when the system has some balance between precision and recall. The value of F1 score can be found in (5).

$$Skor\ F1 = \frac{2 \times Recall \times Presisi}{Recall + Presisi} \quad (5)$$

3. RESULTS AND DISCUSSION

The method used in this study is a classification algorithm with RF algorithm, NN and SVM, it was used to develop a predictive system to analyze and predict the likelihood of heart disease. To get the performance of this classification algorithm use publicly available datasets in the UCI repository with the cardiology dataset. The dataset used has 12 attributes consisting of nominal and numeric data. The target data classes are absence of heart disease and the presence of heart disease. Can be seen in Figure 3. In the dataset used, 11 features are selected which are used to make predictions, as shown in Figure 4.



	Name	Type	Role	Values
1	Age	numeric	feature	
2	Sex	categorical	feature	F, M
3	ChestPainType	categorical	feature	ASY, ATA, NAP, TA
4	RestingBP	numeric	feature	
5	Cholesterol	numeric	feature	
6	FastingBS	categorical	feature	0, 1
7	RestingECG	categorical	feature	LVH, Normal, ST
8	MaxHR	numeric	feature	
9	ExerciseAngina	categorical	feature	N, Y
10	Oldpeak	numeric	feature	
11	ST_Slope	categorical	feature	Down, Flat, Up
12	**HeartDisease**	**categorical**	**target**	**0, 1**

Figure 3. Dataset used

Data instances: 918
Features: 11
Meta attributes: None
Target: Class 'HeartDisease'

	HeartDisease	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope
1	0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up
2	1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat
3	0	37	M	ATA	130	283	0	ST	98	N	0.0	Up
4	1	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat
5	0	54	M	NAP	150	195	0	Normal	122	N	0.0	Up
6	0	39	M	NAP	120	339	0	Normal	170	N	0.0	Up
7	0	45	F	ATA	130	237	0	Normal	170	N	0.0	Up
8	0	54	M	ATA	110	208	0	Normal	142	N	0.0	Up
9	1	37	M	ASY	140	207	0	Normal	130	Y	1.5	Flat
10	0	48	F	ATA	120	284	0	Normal	120	N	0.0	Up
11	0	37	F	NAP	130	211	0	Normal	142	N	0.0	Up
12	1	58	M	ATA	136	164	0	ST	99	Y	2.0	Flat
13	0	39	M	ATA	120	204	0	Normal	145	N	0.0	Up
14	1	49	M	ASY	140	234	0	Normal	140	Y	1.0	Flat
15	0	42	F	NAP	115	211	0	ST	137	N	0.0	Up
16	0	54	F	ATA	120	273	0	Normal	150	N	1.5	Flat
17	1	38	M	ASY	110	196	0	Normal	166	N	0.0	Flat
18	0	43	F	ATA	120	201	0	Normal	165	N	0.0	Up
19	1	60	M	ASY	100	248	0	Normal	125	N	1.0	Flat
20	1	36	M	ATA	120	267	0	Normal	160	N	3.0	Flat
21	0	43	F	TA	100	223	0	Normal	142	N	0.0	Up
22	0	44	M	ATA	120	184	0	Normal	142	N	1.0	Flat
23	0	49	F	ATA	124	201	0	Normal	164	N	0.0	Up

Figure 4. Features used for heart prediction

This system consists of several stages, namely preprocessing to eliminate noisy or redundant data, then classifying it using the RF algorithm, NN, and SVM. After that, validation is carried out to see the performance of the algorithm, namely AUC, CA, F1, precision, and recall from each algorithm in order to get the algorithm with the best accuracy. Doing this experiment using the Orange application with a daset that has 12 thousand consisting of numeric and nominal data. The classification algorithms tested are RF algorithm, NN and SVM. The confusion matrix value calculates the accuracy of the data mining concept or decision support system, serves to analyze whether the classifier is good at recognizing different classes. The following is a confusion matrix of the RF algorithm, NN and SVM.

The RF algorithm in Figure 5 contains 3351+4511 correct predictions and 749+589 incorrect predictions from a total of 9,200 testing data. Thus, the accuracy of this algorithm (precision) can be calculated as 7862/1338*100%=59%. The SVM algorithm in Figure 6 contains 3281+4545 correct predictions and 819+555 incorrect predictions from a total of 9,200 testing data. Thus, the accuracy of this algorithm (precision) can be calculated as 7826/1374*100%=56%. The SVM algorithm in Figure 7 contains 3364+4453 correct predictions and 736+647 incorrect predictions from a total of 9,200 testing data. Thus, the accuracy of this algorithm (precision) can be calculated as 7817/1383*100%=56%.

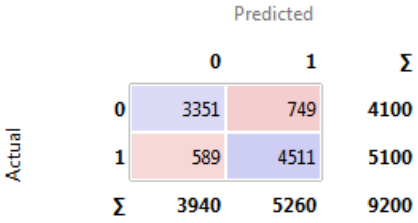


Figure 5. RF confusion matrix

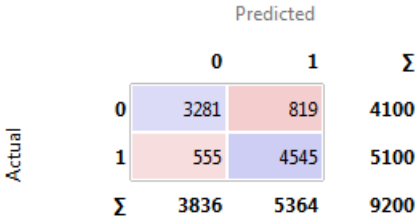


Figure 6. Confusion matrix SVM

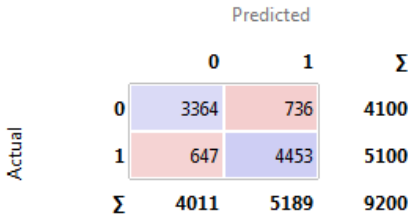


Figure 7. Confusion matrix NN

In Table 2, the value can be seen based on the formula from Table 1. AUC, CA, F1, precision, and recall are the methods used when testing the data. CA can function about the accuracy of the selected dataset. Precision is data accuracy that allows two events, namely 1 and 0. Recall serves to measure the ratio. F1 is the comparison of recall and precision. AUC is used to represent probabilities.

Table 2. Algorithm performance

Model	AUC	CA	F1	Precision	Recall
SVM	0.90	0.85	0.85	0.85	0.85
RF	0.91	0.84	0.84	0.84	0.84
NN	0.90	0.84	0.84	0.84	0.84

In Figure 8, the ROC analysis of each method is marked with a different color graph. RF are marked in Orange, SVMs in green, and NN in gray. In the three methods in one graph, it is clear that the sensitivity is high and specificity values are not more than 1 and when the target class value is changed, in all methods, the changes in sensitivity and specificity are not clearly visible.

From the analysis of the ROC curve in Figures 8 and 9, we can see the performance of the classification algorithm: the closer the curve is to the left and upper limits of the ROC space, the more accurate the classifier is. From the ROC analysis, it can be seen that the SVM model has a slightly better account of the classifier than the NN and RF models. This can be seen in eachclass, it can be seen that the curve of the average SVM approaches the axis or Y axis which indicates that SVM has an optimal classifier accuracy.

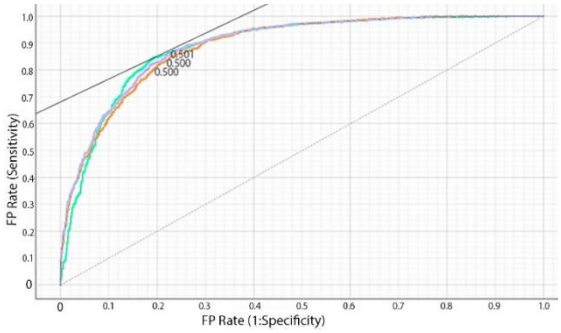


Figure 8. ROC analysis target class 0

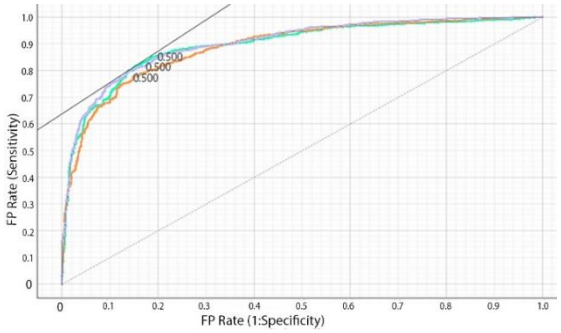


Figure 9. ROC analysis target class 1

4. CONCLUSION

This study evaluates the effectiveness of three device learning algorithms, RF, SVM, and NN in predicting coronary heart disease using a dataset of patients. Via applying information mining strategies with Orange programs and other exploration strategies, the dataset contains attributes with nominal and numeric facts, with the goal magnificence indicating the absence (0) or presence (1) of coronary heart disorder. The comparison consequences reveal that a few of the classification algorithms used SVM, random wooded area, and neural community, the SVM set of rules is the most correct and appropriate for predicting coronary heart sickness, accomplishing an accuracy charge of 85%. Random woodland set of rules excels at coping with complicated and sundry data, successfully lowering the danger of overfitting. Via combining outcomes from a couple of decision bushes, RF affords strong and correct predictions. SVM is particularly powerful in facts class by way of finding the most useful hyperplane that separates information into classes. Its ability to handle abnormal or overlapping statistics makes SVM a reliable tool in coronary heart disease analysis. NN have strong adaptive abilities to apprehend patterns and trends in large and complex datasets. With multiple layers of neurons, this algorithm can provide enormously correct predictions, although it calls for more time and computational sources. Integrating these 3 algorithms right into a heart sickness prediction gadget not handiest complements diagnostic accuracy but also aids in higher clinical choice-making. Using machine mastering in healthcare holds massive capacity for decreasing human errors, enhancing performance, and handing over better fitness effects for patients.

Even though SVM indicates the fine performance on this have a look at, there are several regions for in addition exploration. First, destiny studies could include evaluating newer algorithms or combining algorithms (ensemble methods) to look if accuracy can be improved. Second, including more attributes or variables to the dataset could enhance prediction nice. Subsequently, similarly studies have to do not forget the interpretability of models to ensure that prediction consequences can be understood and relied on by way of clinical practitioners in medical selection-making.

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